



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/019,151A  
Source: P9/10  
Date Processed by STIC: 2/19/04

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT**

**MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221**

**Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03



PCT

## RAW SEQUENCE LISTING

DATE: 02/25/2004

PATENT APPLICATION: US/10/019,151A

TIME: 08:52:43

Input Set : A:\01997.025700.txt

Output Set: N:\CRF4\02252004\J019151A.raw

3 &lt;110&gt; APPLICANT: Sagami Chemical Research Center, Protegene Inc.

5 &lt;120&gt; TITLE OF INVENTION: Human proteins having hydrophobic domains and DNAs encoding these proteins

7 &lt;130&gt; FILE REFERENCE: 661924

9 &lt;140&gt; CURRENT APPLICATION NUMBER: US/10/019,151A

10 &lt;141&gt; CURRENT FILING DATE: 2003-01-31

12 &lt;150&gt; PRIOR APPLICATION NUMBER: JP 11-178065

13 &lt;151&gt; PRIOR FILING DATE: 1999-06-24

15 &lt;160&gt; NUMBER OF SEQ ID NOS: 24

Please ensure that  
file is saved in  
ASCII text,

## ERRORED SEQUENCES

17 &lt;210&gt; SEQ ID NO: 1

18 &lt;211&gt; LENGTH: 238

19 &lt;212&gt; TYPE: PRT

20 &lt;213&gt; ORGANISM: Homo sapiens

22 &lt;400&gt; SEQUENCE: 1

23 Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val Asp Met

24 1 5 10 15

25 Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe Thr Gly

26 20 25 30

27 Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu Lys Thr

28 35 40 45

29 Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu Gln Val

30 50 55 60

31 Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn Ala Leu

32 65 70 75 80

33 Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn Lys Gly

34 85 90 95

35 Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met Asp Ile

36 100 105 110

37 Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr Leu Phe

38 115 120 125

39 Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His Thr His

40 130 135 140

41 Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn Thr Glu

42 145 150 155 160

43 Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu Ile Val

E--&gt; 44 165 165 ← goes under Gln 170 175

45 Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu Leu Ile

E--&gt; 46 180 185 190

47 Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His Cys Ala

E--&gt; 48 195 200 205

Does Not Comply  
Corrected Diskette Needed

pp 1, 3-8

per  
Sequence  
Rules.

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Input Set : A:\01997.025700.txt

Output Set: N:\CRF4\02252004\J019151A.raw

49 Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys Met Gly  
 50 210 215 220  
 51 Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser  
 52 225 230 235  
 54 <210> SEQ ID NO: 2  
 55 <211> LENGTH: 339  
 56 <212> TYPE: PRT  
 57 <213> ORGANISM: Homo sapiens  
 59 <400> SEQUENCE: 2  
 60 Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu  
 61 1 5 10 15  
 62 Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn  
 63 20 25 30  
 64 Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His  
 65 35 40 45  
 66 Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu  
 67 50 55 60  
 68 Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val  
 69 65 70 75 80  
 70 Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu  
 71 85 90 95  
 72 Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val  
 73 100 105 110  
 74 Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly  
 75 115 120 125  
 76 Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln  
 77 130 135 140  
 78 Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp  
 79 145 150 155 160  
 80 Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu  
 81 165 170 175  
 82 Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu  
 83 180 185 190  
 84 Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro  
 85 195 200 205  
 86 Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro  
 87 210 215 220  
 88 Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His  
 89 225 230 235 240  
 90 Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr  
 91 245 250 255  
 92 Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile  
 93 260 265 270  
 94 Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp  
 95 275 280 285  
 96 Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn  
 97 290 295 300  
 98 Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys  
 99 305 310 315 320

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Input Set : A:\01997.025700.txt

Output Set: N:\CRF4\02252004\J019151A.raw

E--> 100 Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr  
 101 325 330 336  
 102 Arg Arg Arg 335

255 &lt;210&gt; SEQ ID NO: 7

256 &lt;211&gt; LENGTH: 200

257 &lt;212&gt; TYPE: PRT

258 &lt;213&gt; ORGANISM: Homo sapiens

260 &lt;400&gt; SEQUENCE: 7

E--> 261 Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala  
 262 1 5 10 15  
 263 Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp  
 264 20 25 30  
 265 Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe  
 266 35 40 45  
 267 Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg  
 268 50 55 60  
 269 Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu  
 270 65 70 75 80  
 271 Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val  
 272 85 90 95  
 273 Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe  
 274 100 105 110  
 275 Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser  
 276 115 120 125  
 277 Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val  
 278 130 135 140  
 279 Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys  
 280 145 150 155 160  
 281 Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met  
 282 165 170 175  
 283 Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr  
 284 180 185 190  
 285 Leu Glu Lys Thr Ile His Glu Glu  
 286 195 200

386 &lt;210&gt; SEQ ID NO: 12

387 &lt;211&gt; LENGTH: 972

388 &lt;212&gt; TYPE: DNA

389 &lt;213&gt; ORGANISM: Homo sapiens

391 &lt;400&gt; SEQUENCE: 12

OK 392 atggcgcccg cggtccggg gaacggccgc gcacggcgcc cccggctgct tctgctcttt 60  
 393 ctggttcgc tgctgtgggc cccggctgcg gtccgggccc gccagatga agaccttagc 120  
 394 caccggaaca aagaaccgcc ggcgcgggcc cagcagctgc agccgcagcc tgtggtgtg 180  
 395 cagggccccc agccggcccc ggtcgagaaa atatttacac cagcagctcc agttcatacc 240  
 396 aataaagaag atcctgctac ccaaactaat ttgggattta tccatgcatt tgcgtgtgcc 300  
 397 atatcagtta ttattgtatc tgaattgggt gataagacat tttttatagc agccatcatg 360  
 398 gcaatgcgct ataaccgcct gaccgtgctg gctggtgcaa tgcttgccct gggactaatg 420  
 399 acatgcttgt cagttttgtt tggctatgcc accacagtca tcccagggt ctatacatc 480  
 400 tatgtttcaa ctgtattatt tgcaattttt ggcattagaa tgcttcggga aggcttaag 540  
 401 atgagccctg atgagggtca agaggaactg gaagaagttc aagctgaatt aaagaagaaa 600

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Input Set : A:\01997.025700.txt

Output Set: N:\CRF4\02252004\J019151A.raw

W--&gt; 402

gatgaagaat ttcaacgaac caaactttta aatggaccgg gagatgttga aacgggtaca 660 agcataacag tacctcagaa aa

E--&gt; 403

a ctgtggggca ctgcctgtgc 840 acgggattgg cagtaattgg aggaagaatg atagcacaga aaatctctgt cagaactgtg

E--&gt; 404 gattctgggtt tt

972

792 &lt;210&gt; SEQ ID NO: 21

793 &lt;211&gt; LENGTH: 2064

794 &lt;212&gt; TYPE: DNA

795 &lt;213&gt; ORGANISM: Homo sapiens

797 &lt;220&gt; FEATURE:

798 &lt;221&gt; NAME/KEY: CDS

799 &lt;222&gt; LOCATION: (98)...(559)

801 &lt;400&gt; SEQUENCE: 21

E--&gt; 802 aaaacagctg ctggagcagc agcggccccc gctcccgga accgttcccg ggcggtgat 60

803 cttcggcccc acacgaacag cagagagggg cagcagg atg aat gtg ggc aca 112

804 Met Asn Val Gly Thr

805 1 5

806 gcg cac agc gag gtg aac ccc aac acg cgg gtg atg aac agc cgt ggc 160

807 Ala His Ser Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly

808 10 15 20

809 atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc ctc cac atc gtg ctg 208

810 Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu Leu His Ile Val Leu

811 25 30 35

812 ctg agc atc ccg ttt gtg agt gtc cct gtc gtc tgg acc ctc acc aac 256

813 Leu Ser Ile Pro Phe Val Ser Val Pro Val Val Trp Thr Leu Thr Asn

814 40 45 50

815 ctc att cac aac atg ggc atg tat atc ttc ctg cac acg gtg aag ggg 304

816 Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu His Thr Val Lys Gly

817 55 60 65

818 aca ccc ttt gag acc ccg gac cag ggc aag gcg agg ctg cta acc cac 352

819 Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His

820 70 75 80 85

821 tgg gag cag atg gat tat ggg gtc cag ttc acg gcc tct cgg aag ttc 400

822 Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr Ala Ser Arg Lys Phe

823 90 95 100

824 ttg acc atc aca ccc atc gtg ctg tac ttc ctc acc agc ttc tac act 448

825 Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu Thr Ser Phe Tyr Thr

826 105 110 115

827 aag tac gac cag atc cat ttt gtg ctc aac acc gtg tcc ctg atg agc 496

828 Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr Val Ser Leu Met Ser

829 120 125 130

830 gtg ctt atc ccc aag ctg ccc cag ctc cac gga gtc cgg att ttt gga 544

831 Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly Val Arg Ile Phe Gly

832 135 140 145

833 atc aat aag tac tgagagtga gcccttccc ctgccaggg tggcagggga gggg 600

834 Ile Asn Lys Tyr

835 150

836 tagggtaaaa ggcattgtgt gcaacactga agacagaaag aagaagcctc tggacactgc 660

837 cagagatggg ggttgagcct ctggcctaatt ttccccctc gcttccccca gtagccaact 720

838 tggagtagct tgtagtgggg ttgggtagg cccctgggc tctgaccttt tctgaatttt 780

839 ttgatctttt ctttttgctt ttggaataga gactccatgg agttggtcat ggaatgggct 840

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TIME: 08:52:43

Input Set : A:\01997.025700.txt

Output Set: N:\CRF4\02252004\J019151A.raw

840 gggctcctgg gctgaacatg gaccacgcag ttgcgacagg aggccagggg aaaaaccctt 900  
 841 gctcacttgt ttgccctcag gcagccaaag cactttaacc cctgcatagg gagcagaggg 960  
 W--> 842 *insert hard return*  
 cggtacgggt tctggattgt ttcactgtga ttcctagggt ttttcgatgc caccagctgt 1020 gtgcttttgt gtatggaagc aa  
 W--> 843  
 g tagatggctt ggttccagag 1200 *g*tgagggggc cagggtgct gccatcctgg cctggtggag gttggggagc tgtaggagag  
 E--> 844 caggcttga gggtaattt acccacagaa tgtgatagta ataggggagg gaggtgctg 1440  
 E--> 845 tgggtttaac tctgggttg gctgttgggt agacagggtg ggaaaaggcc cgtgagtcac 1500  
 E--> 846 tgtaagcaca ggtccaactt ggccctgact cctgcggggg tatggggaag ctgtgacaga 1560  
 E--> 847 aacgatgggt gctgtgtgct tctgcaggcc ctcacccctt aacttcctca tacagactgg 1620  
 E--> 848 cactgggcag ggctctctcat gtggcagcca catgtggcgt tgtgaggcca ccccatgtgg 1680  
 E--> 849 ggtctgtggt gagagtctgt taggatccct gctcaagcag cacagaggaa ggggcaagac 1740  
 E--> 850 gtggcctgta ggcactgttt cagcctgcag agaagaaagt gaggcggga gctgagcct 1800  
 E--> 851 gggctggagc cttctccctt cccagttgg actaggggca gtgttaattt tgaaaagggtg 1860  
 E--> 852 tgggtccctg tgtcctcttc cagggttcca aggggaacagg agaggtcact gggcctgttt 1920  
 E--> 853 tctccctcct gaccctgcac ctcacccccc gtgtatcata gggaaacttt accttaaaat 1980  
 E--> 854 cttttotaagc aaagtgtgaa taggattttt actccctttg tacagtattc tgagaaacgc 2040  
 E--> 855 aaataaaagg gcaacatggt tctg 2064  
 902 <210> SEQ ID NO: 23  
 903 <211> LENGTH: 1161  
 904 <212> TYPE: DNA  
 905 <213> ORGANISM: Homo sapiens  
 907 <220> FEATURE:  
 908 <221> NAME/KEY: CDS  
 909 <222> LOCATION: (278)... (880)  
 911 <400> SEQUENCE: 23  
 Q--> 912 acatgagcca ccaaaatggt ggtgttcggg tatgaggctg ggactaagcc aagggtatca 60  
 913 ggtgtggtgc cggtgggaac tgaggaagcg cccaaggaaa tgaaacacga tttccaaaat 120  
 914 gaacttaate tttcatgaga aactgaggat agagatgtca ataagcagcc actgtttcca 180  
 915 cctccccacc tgaagagcta ggaggacaac tacaaagagc ctgactgcct tctcggaatg 240  
 916 aggagagagg aaaacagcaa cagtatcagt tttcaag atg gca gca tct atg 292  
 917 Met Ala Ala Ser Met  
 918 1 5  
 919 cat ggt cag ccc agt cct tct cta gaa gat gca aaa ctc aga aga cca 340  
 920 His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu Arg Arg Pro  
 921 10 15 20  
 922 atg gtc ata gaa atc ata gaa aaa aat ttt gac tat ctt aga aaa gaa 388  
 923 Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp Tyr Leu Arg Lys Glu  
 924 25 30 35  
 925 atg aca caa aat ata tat caa atg gcg aca ttt gga aca aca gct ggt 436  
 926 Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr Thr Ala Gly  
 927 40 45 50  
 928 ttc tct gga ata ttc tca aac ttc ctg ttc aga cgc tgc ttc aag gtt 484  
 929 Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys Phe Lys Val  
 930 55 60 65  
 931 aaa cat gat gct ttg aag aca tat gca tca ttg gct aca ctt cca ttt 532  
 932 Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr Leu Pro Phe  
 933 70 75 80 85  
 934 ttg tct act gtt gtt act gac aag ctt ttt gta att gat gct ttg tat 580  
 935 Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp Ala Leu Tyr  
 936 90 95 100

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DATE: 02/25/2004

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TIME: 08:52:43

Input Set : A:\01997.025700.txt

Output Set: N:\CRF4\02252004\J019151A.raw

```

937 tca gat aat ata agc aag gaa aac tgt gtt ttc aga agc tca ctg att      628
938 Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser Ser Leu Ile
939          105          110          115
940 ggc ata gtt tgt ggt gtt ttc tat ccc agt tct ttg gct ttt act aaa      676
941 Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala Phe Thr Lys
942          120          125          130
943 aat gga cgc ctg gca acc aag tat cat acc gtt cca ctg cca cca aaa      724
944 Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val Pro Leu Pro Pro Lys
945          135          140          145
946 gga agg gtt tta atc cat tgg atg acg ctt tgt caa aca caa atg aaa      772
947 Gly Arg Val Leu Ile His Trp Met Thr Leu Cys Gln Thr Gln Met Lys
948 150          155          160          165
949 tta atg gcg att cct cta gtc ttt cag att atg ttt gga ata tta aat      820
950 Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met Phe Gly Ile Leu Asn
951          170          175          180
952 ggt cta tac cat tat gca gta ttt gaa gag aca ctt gag aaa act ata      868
953 Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr Leu Glu Lys Thr Ile
954          185          190          195
955 cat gaa gag taaccaaaaa aatgaatggt tgctaactta gcaaaatgaa gtt      920
956 His Glu Glu
957          200
958 tctataaaga ggactcaggc attgctgaaa gagttaaaag taactgtgaa caaataattt  980
W--> 959
gtttctgtgcc ttttgccctgg tatatagcaa atactcaaaa agtattcaat aattcaatca 1040 ataaatataa gtttcatott ac
E--> 960 t

```

↑  
Insert  
hard  
return

10/019,151A

7

<210> 17  
 <211> 1167  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (187)...(903)

<400> 17  
 cttgcctctg ggaaggaaat acattataga gtgggaaatt tttatcattt tgaaccaaga 60  
 ttctttctaaa gaaagaaaga ctgattaata aaatgtggca gctgtgctct tcaaggcatt 120  
 tatagtgtat atagtttttag aaaaacagtc ccaccactta agcatagatg taatttacta 180  
 ataaaa atg att ctg ctt gtg att ctt gca ttt tat ctg tgg cag gtg 228  
 Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val  
 1 5 10  
 gac atg ttg agt gaa att aac att gct ccc cgg att ctc acc aat ttc 276  
 Asp Met Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe  
 15 20 25 30  
 act gga gta atg cca cct cag ttc aaa aag gat ttg gat tcc tat ctt 324  
 Thr Gly Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu  
 35 40 45  
 aaa act cga tca cca gtc act ttc ctg tct gat ctg cgc agc aac cta 372  
 Lys Thr Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu  
 50 55 60

fix numbering →



from seq. 18

10/01/151A 8

tgt	gaa	ggc	tat	gag	tcc	tct	gaa	gac	cag	tat	gta	cta	aga	ggg	tct	501
Cys	Glu	Gly	Tyr	Glu	Ser	Ser	Glu	Asp	Gln	Tyr	Val	Leu	Arg	Gly	Ser	
115					<del>120</del>	120					125					

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/019,151A

DATE: 02/25/2004  
TIME: 08:52:44

Input Set : A:\01997.025700.txt  
Output Set: N:\CRF4\02252004\J019151A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5  
Seq#:12; Line(s) 402,403  
Seq#:21; Line(s) 842,843  
Seq#:23; Line(s) 959

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/019,151A

DATE: 02/25/2004

TIME: 08:52:44

Input Set : A:\01997.025700.txt

Output Set: N:\CRF4\02252004\J019151A.raw

L:44 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1  
M:332 Repeated in SeqNo=1  
L:101 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
L:261 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
L:402 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:12  
L:402 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:19  
L:403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12  
L:403 M:254 E: No. of Bases conflict, LENGTH:Input:960 Counted:741 SEQ:12  
L:403 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6  
M:254 Repeated in SeqNo=12  
L:404 M:252 E: No. of Seq. differs, <211> LENGTH:Input:972 Found:753 SEQ:12  
L:491 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:497 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:500 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:503 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:506 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:509 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:512 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:515 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:518 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:521 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:524 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:527 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:571 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:574 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:577 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:580 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:583 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:586 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:589 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:592 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:595 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:598 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:601 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:604 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:607 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:610 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:614 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18  
L:842 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:21  
L:843 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:21  
L:842 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:19  
L:843 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21  
L:843 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:20  
L:844 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21  
L:844 M:254 E: No. of Bases conflict, LENGTH:Input:1440 Counted:1020 SEQ:21  
M:254 Repeated in SeqNo=21  
L:855 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2064 Found:1644 SEQ:21

**VERIFICATION SUMMARY**

DATE: 02/25/2004

PATENT APPLICATION: US/10/019,151A

TIME: 08:52:44

Input Set : A:\01997.025700.txt

Output Set: N:\CRF4\02252004\J019151A.raw

L:959 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:23  
L:959 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:19  
L:960 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:960 M:254 E: No. of Bases conflict, LENGTH:Input:1161 Counted:981 SEQ:23  
L:960 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1161 Found:981 SEQ:23